|	
CALGENE LLC,	)
	)
Claimant,	)
	)
v.	) No. 50 T 153 00190 99
	)
RHÔNE-POULENC AGRO S.A.	)
	)
Respondent.	)

DECLARATION

We, Alain Sailland, PhD and Jean-Marc Ferrullo, PhD, hereby declare under penalty of perjury that the facts set forth in the Report "Comparison of Glyphosate Tolerance of Four Coding Sequences in Transgenic Tobacco" are true and correct of our knowledge, and, if called as witnesses, we could and would testify competently that the Report is true and accurate.

We make this Declaration under the penalty of perjury under the laws of the United States, that all of the above statements are made of our own knowledge and are true and correct to the best of our belief. This Declaration is executed this 3th day of April, 2001

Alain Sailland, PhD

Jean-Marc Ferrullo, PhD

Exhibit 1
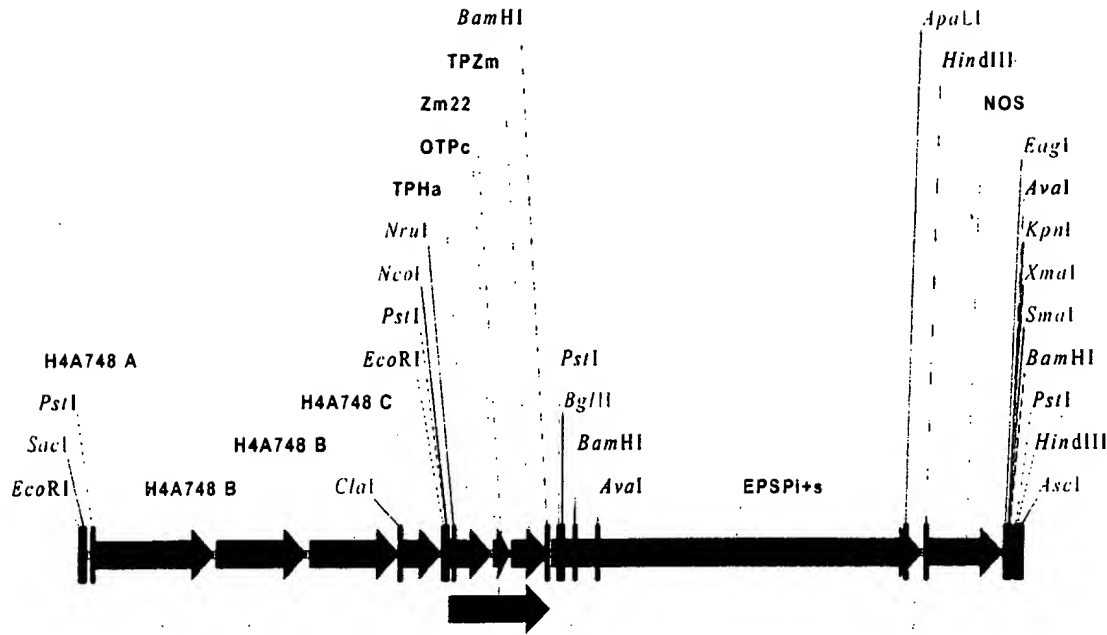
Fragment of pRD 2010-sac
3381 bp (molecule 6076 bp)

Coding sequence for pRD 2010-sac :

```
          M   A   S   I   S   S   S   V   A   T   V   S   R   T   A   P   A   Q   A   N   M   V   A   P
4065   ATGGCTTCGATC TCCTCCTCAGTC GCGACCGTTAGC CGGACCGCCCCT GCTCAGGCCAAC ATGGTGGCTCCG
          F   T   G   L   K   S   N   A   A   F   P   T   T   K   K   A   N   D   F   S   T   L   P   S
4137   TTCACCGGCCTT AAGTCCAACGCC GCCTTCCCCACC ACCAAGAAGGCT AACGACTTCTCC ACCCTTCCCAGC
          N   G   G   R   V   Q   C   M   Q   V   W   P   A   Y   G   N   K   K   F   E   T   L   S   Y
4209   AACGGTGGAAGA GTTCAATGTATG CAGGTGTGGCCG GCCTACGGCAAC AAGAAGTTCGAG ACGCTGTCGTAC
          L   P   P   L   S   M   A   P   T   V   M   M   A   S   S   T   A   V   A   P   F   Q   G
4281   CTGCCGCCGCTG TCTATGGCGCCC ACCGTGATGATG GCCTCGTCGGCC ACCGCCGTCGCT CCGTTCCAGGGG
          L   K   S   T   A   S   L   P   V   A   R   R   S   S   R   S   L   G   N   V   S   N   G   G
4353   CTCAAGTCCACC GCCAGCCTCCCC GTCGCCCGCCGC TCCTCCAGAAGC CTCGGCAACGTC AGCAACGGCGGA
          R   I   R   C   M   A   G   A   E   E   I   V   L   Q   P   I   K   E   I   S   G   T   V   K
4425   AGGATCCGGTGC ATGGCCGGCGCC GAGGAGATCGTG CTGCAGCCCATC AAGGAGATCTCC GGCACCGTCAAG
          L   P   G   S   K   S   L   S   N   R   I   L   L   L   A   A   L   S   E   G   T   T   V   V
4497   CTGCCGGGGTCC AAGTCGCTTTCC AACCGGATCCTC CTACTCGCCGCC CTGTCCGAGGGG ACAACAGTGGTT
          D   N   L   L   N   S   E   D   V   H   Y   M   L   G   A   L   R   T   L   G   L   S   V   E
4569   GATAACCTGCTG AACAGTGAGGAT GTCCACTACATG CTCGGGGCCTTG AGGACTCTTGGT CTCTCTGTCGAA
          A   D   K   A   A   K   R   A   V   V   V   G   C   G   G   K   F   P   V   E   D   A   K   E
4641   GCGGACAAAGCT GCCAAAAGAGCT GTAGTTGTTGGC TGTGGTGGAAAG TTCCCAGTTGAG GATGCTAAAGAG
          E   V   Q   L   F   L   G   N   A   G   I   A   M   R   S   L   T   A   A   V   T   A   A   G
4713   GAAGTGCAGCTC TTCTTGGGGAAT GCTGGAATCGCA ATGCGGTCCTTG ACAGCAGCTGTT ACTGCTGCTGGT
          G   N   A   T   Y   V   L   D   G   V   P   R   M   R   E   R   P   I   G   D   L   V   V   G
4785   GGAAATGCAACT TACGTGCTTGAT GGAGTACCAAGA ATGAGGGAGAGA CCCATTGGCGAC TTGGTTGTCGGA
          L   K   Q   L   G   A   D   V   D   C   F   L   G   T   D   C   P   P   V   R   V   N   G   I
4857   TTGAAGCAGCTT GGTGCAGATGTT GATTGTTTCCTT GGCACTGACTGC CCACCTGTTCGT GTCAATGGAATC
          G   G   L   P   G   G   K   V   K   L   S   G   S   I   S   S   Q   Y   L   S   A   L   L   M
4929   GGAGGGCTACCT GGTGGCAAGGTC AAGCTGTCTGGC TCCATCAGCAGT CAGTACTTGAGT GCCTTGCTGATG
          A   A   P   L   A   L   G   D   V   E   I   E   I   I   D   K   L   I   S   I   P   Y   V   E
5001   GCTGCTCCTTTG GCTCTTGGGGAT GTGGAGATTGAA ATCATTGATAAA TTAATCTCCATT CCGTACGTCGAA
          M   T   L   R   L   M   E   R   F   G   V   K   A   E   H   S   D   S   W   D   R   F   Y   I
5073   ATGACATTGAGA TTGATGGAGCGT TTTGGTGTGAAA GCAGAGCATTCT GATAGCTGGGAC AGATTCTACATT
          K   G   G   Q   K   Y   K   S   P   K   N   A   Y   V   E   G   D   A   S   S   A   S   Y   F
5145   AAGGGAGGTCAA AAATACAAGTCC CCTAAAAATGCC TATGTTGAAGGT GATGCCTCAAGC GCAAGCTATTTC
          L   A   G   A   A   I   T   G   G   T   V   T   V   E   G   C   G   T   T   S   L   Q   G   D
5217   TTGGCTGGTGCT GCAATTACTGGA GGGACTGTGACT GTGGAAGGTTGT GGCACCACCAGT TTGCAGGGTGAT
          V   K   F   A   E   V   L   E   M   M   G   A   K   V   T   W   T   E   T   S   V   T   V   T
5289   GTGAAGTTTGCT GAGGTACTGGAG ATGATGGGAGCG AAGGTTACATGG ACCGAGACTAGC GTAACTGTTACT
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      G   P   P   R    E   P   F   G    R   K   H   L    K   A   I   D    V   N   M   N    K   M   P   D
5361  GGCCCACCGCGG GAGCCATTTGGG AGGAAACACCTC AAGGCGATTGAT GTCAACATGAAC AAGATGCCTGAT
      V   A   M   T    L   A   V   V    A   L   F   A    D   G   P   T    A   I   R   D    V   A   S   W
5433  GTCGCCATGACT CTTGCTGTGGTT GCCCTCTTTGCC GATGGCCCGACA GCCATCAGAGAC GTGGCTTCCTGG
      R   V   K   E    T   E   R   M    V   A   I   R    T   E   L   T    K   L   G   A    S   V   E   E
5505  AGAGTAAAGGAG ACCGAGAGGATG GTTGCGATCCGG ACGGAGCTAACC AAGCTGGGAGCA TCTGTTGAGGAA
      G   P   D   Y    C   I   I   T    P   P   E   K    L   N   V   T    A   I   D   T    Y   D   D   H
5577  GGGCCGGACTAC TGCATCATCACG CCGCCGGAGAAG CTGAACGTGACG GCGATCGACACG TACGACGACCAC
      R   M   A   M    A   F   S   L    A   A   C   A    E   V   P   V    T   I   R   D    P   G   C   T
5649  AGGATGGCGATG GCTTTCTCCCTT GCCGCCTGTGCC GAGGTCCCCGTC ACCATCCGGGAC CCTGGGTGCACC
      R   K   T   F    P   D   Y   F    D   V   L   S    T   F   V   K    N
5721  CGGAAGACCTTC CCCGACTACTTC GATGTGCTGAGC ACTTTCGTCAAG AAT
```
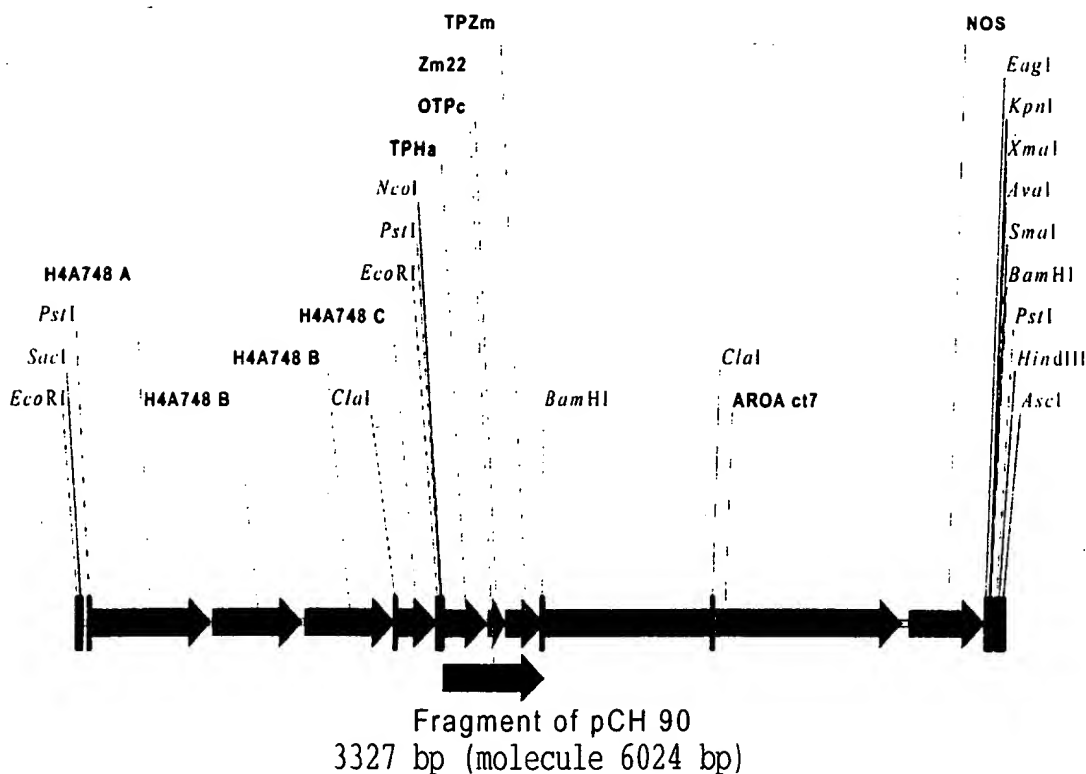
Exhibit 2
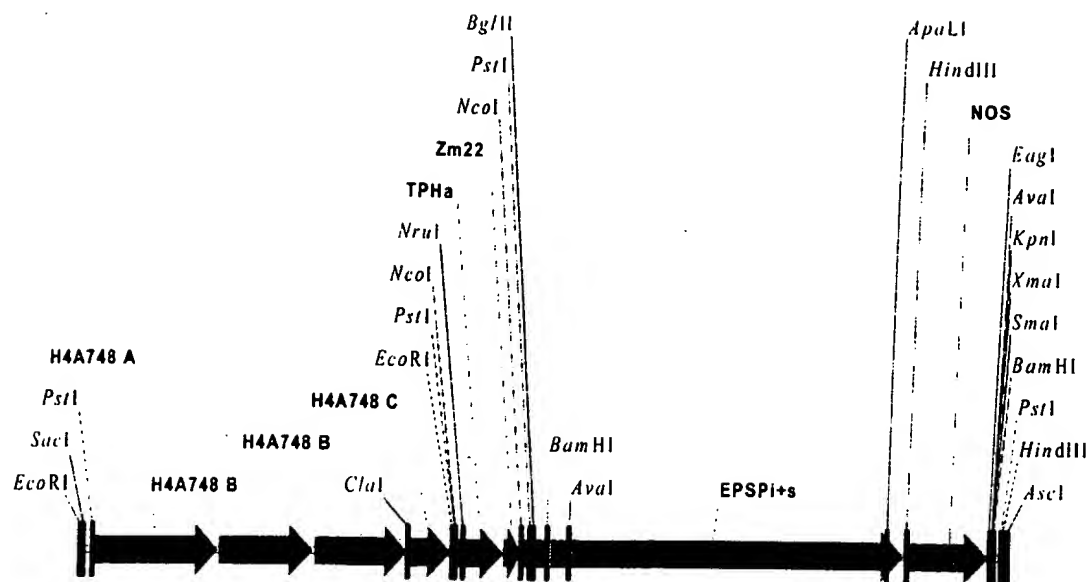
Fragment of pEPS2
3240 bp (molecule 5935 bp)

Coding sequence for pEPS2

```
       M   A   S   I    S   S   S   V    A   T   V   S    R   T   A   P    A   Q   A   N    M   V   A   P
5664   ATGGCTTCGATC TCCTCCTCAGTC GCGACCGTTAGC CGGACCGCCCCT GCTCAGGCCAAC ATGGTGGCTCCG
       F   T   G   L    K   S   N   A    A   F   P   T    T   K   K   A    N   D   F   S    T   L   P   S
5736   TTCACCGGCCTT AAGTCCAACGCC GCCTTCCCCACC ACCAAGAAGGCT AACGACTTCTCC ACCCTTCCCAGC
       N   G   G   R    V   Q   C   M    Q   V   W   P    A   Y   G   N    K   K   F   E    T   L   S   Y
5808   AACGGTGGAAGA GTTCAATGTATG CAGGTGTGGCCG GCCTACGGCAAC AAGAAGTTCGAG ACGCTGTCGTAC
       L   P   P   L    S   M   A   G    A   E   E   I    V   L   Q   P    I   K   E   I    S   G   T   V
5880   CTGCCGCCGCTG TCCATGGCCGGC GCCGAGGAGATC GTGCTGCAGCCC ATCAAGGAGATC TCCGGCACCGTC
       K   L   P   G    S   K   S   L    S   N   R   I    L   L   L   A    A   L   S   E    G   T   T   V
17     AAGCTGCCGGGG TCCAAGTCGCTT TCCAACCGGATC CTCCTACTCGCC GCCCTGTCCGAG GGGACAACAGTG
       V   D   N   L    L   N   S   E    D   V   H   Y    M   L   G   A    L   R   T   L    G   L   S   V
89     GTTGATAACCTG CTGAACAGTGAG GATGTCCACTAC ATGCTCGGGGCC TTGAGGACTCTT GGTCTCTCTGTC
       E   A   D   K    A   A   K   R    A   V   V   V    G   C   G   G    K   F   P   V    E   D   A   K
161    GAAGCGGACAAA GCTGCCAAAAGA GCTGTAGTTGTT GGCTGTGGTGGA AAGTTCCCAGTT GAGGATGCTAAA
       E   E   V   Q    L   F   L   G    N   A   G   I    A   M   R   S    L   T   A   A    V   T   A   A
233    GAGGAAGTGCAG CTCTTCTTGGGG AATGCTGGAATC GCAATGCGGTCC TTGACAGCAGCC GTTACTGCTGCT
       G   G   N   A    T   Y   V   L    D   G   V   P    R   M   R   E    R   P   I   G    D   L   V   V
305    GGTGGAAATGCA ACTTACGTGCTT GATGGAGTACCA AGAATGAGGGAG AGACCCATTGGC GACTTGGTTGTC
       G   L   K   Q    L   G   A   D    V   D   C   F    L   G   T   D    C   P   P   V    R   V   N   G
377    GGATTGAAGCAG CTTGGTGCAGAT GTTGATTGTTTC CTTGGCACTGAC TGCCCACCTGTT CGTGTCAATGGA
       I   G   G   L    P   G   G   K    V   K   L   S    G   S   I   S    S   Q   Y   L    S   A   L   L
449    ATCGGAGGGCTA CCTGGTGGCAAG GTCAAGCTGTCT GGCTCCATCAGC AGTCAGTACTTG AGTGCCTTGCTG
       M   A   A   P    L   A   L   G    D   V   E   I    E   I   I   D    K   L   I   S    I   P   Y   V
521    ATGGCTGCTCCT TTGGCTCTTGGG GATGTGGAGATT GAAATCATTGAT AAATTAATCTCC ATTCCGTACGTC
       E   M   T   L    R   L   M   E    R   F   G   V    K   A   E   H    S   D   S   W    D   R   F   Y
593    GAAATGACATTG AGATTGATGGAG CGTTTTGGTGTG AAAGCAGAGCAT TCTGATAGCTGG GACAGATTCTAC
       I   K   G   G    Q   K   Y   K    S   P   K   N    A   Y   V   E    G   D   A   S    S   A   S   Y
665    ATTAAGGGAGGT CAAAAATACAAG TCCCCTAAAAAT GCCTATGTTGAA GGTGATGCCTCA AGCGCAAGCTAT
       F   L   A   G    A   A   I   T    G   G   T   V    T   V   E   G    C   G   T   T    S   L   Q   G
737    TTCTTGGCTGGT GCTGCAATTACT GGAGGGACTGTG ACTGTGGAAGGT TGTGGCACCACC AGTTTGCAGGGT
       D   V   K   F    A   E   V   L    E   M   M   G    A   K   V   T    W   T   E   T    S   V   T   V
809    GATGTGAAGTTT GCTGAGGTACTG GAGATGATGGGA GCGAAGGTTACA TGGACCGAGACT AGCGTAACTGTT
       T   G   P   P    R   E   P   F    G   R   K   H    L   K   A   I    D   V   N   M    N   K   M   P
881    ACTGGCCCACCG CGGGAGCCATTT GGGAGGAAACAC CTCAAGGCGATT GATGTCAACATG AACAAGATGCCT
       D   V   A   M    T   L   A   V    V   A   L   F    A   D   G   P    T   A   I   R    D   V   A   S
953    GATGTCGCCATG ACTCTTGCTGTG GTTGCCCTCTTT GCCGATGGCCCG ACAGCCATCAGA GACGTGGCTTCC
       W   R   V   K    E   T   E   R    M   V   A   I    R   T   E   L    T   K   L   G    A   S   V   E
1025   TGGAGAGTAAAG GAGACCGAGAGG ATGGTTGCGATC CGGACGGAGCTA ACCAAGCTGGGA GCATCTGTTGAG
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            E  G  P  D    Y  C  I  I    T  P  P  E    K  L  N  V    T  A  I  D    T  Y  D  D
1097   GAAGGGCCGGAC TACTGCATCATC ACGCCGCCGGAG AAGCTGAACGTG ACGGCGATCGAC ACGTACGACGAC
            H  R  M  A    M  A  F  S    L  A  A  C    A  E  V  P    V  T  I  R    D  P  G  C
1169   CACAGGATGGCG ATGGCTTTCTCC CTTGCCGCCTGT GCCGAGGTCCCC GTCACCATCCGG GACCCTGGGTGC
            T  R  K  T    F  P  D  Y    F  D  V  L    S  T  F  V    K  N
1241   ACCCGGAAGACC TTCCCCGACTAC TTCGATGTGCTG AGCACTTTCGTC AAGAAT
```
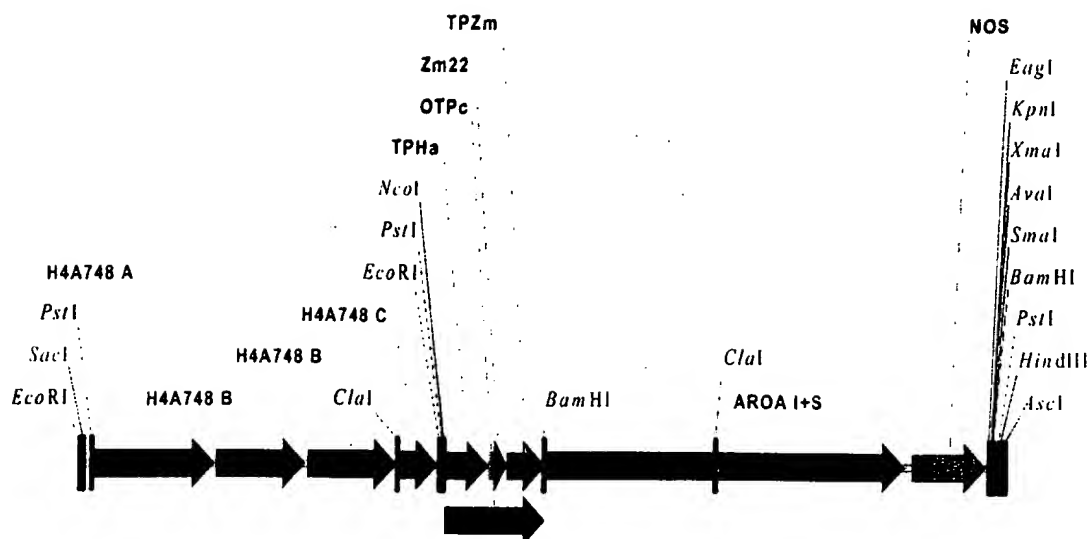
Exhibit 3

Fragment of pCH 90
3327 bp (molecule 6024 bp)

Coding sequence for pCH90:

```
          M   A   S   I   S   S   S   V   A   T   V   S   R   T   A   P   A   Q   A   N   M   V   A   P
4065   ATGGCTTCGATC TCCTCCTCAGTC GCGACCGTTAGC CGGACCGCCCCT GCTCAGGCCAAC ATGGTGGCTCCG
          F   T   G   L   K   S   N   A   A   F   P   T   T   K   K   A   N   D   F   S   T   L   P   S
4137   TTCACCGGCCTT AAGTCCAACGCC GCCTTCCCCACC ACCAAGAAGGCT AACGACTTCTCC ACCCTTCCCAGC
          N   G   G   R   V   Q   C   M   Q   V   W   P   A   Y   G   N   K   K   F   E   T   L   S   Y
4209   AACGGTGGAAGA GTTCAATGTATG CAGGTGTGGCCG GCCTACGGCAAC AAGAAGTTCGAG ACGCTGTCGTAC
          L   P   P   L   S   M   A   P   T   V   M   M   A   S   S   A   T   A   V   A   P   F   Q   G
4281   CTGCCGCCGCTG TCTATGGCGCCC ACCGTGATGATG GCCTCGTCGGCC ACCGCCGTCGCT CCGTTCCAGGGG
          L   K   S   T   A   S   L   P   V   A   R   R   S   S   R   S   L   G   N   V   S   N   G   G
4353   CTCAAGTCCACC GCCAGCCTCCCC GTCGCCCGCCGC TCCTCCAGAAGC CTCGGCAACGTC AGCAACGGCGGA
          BamHI
          ------
          R   I   R   C   M   E   S   L   T   L   Q   P   I   A   R   V   D   G   A   I   N   L   P   G
4425   AGGATCCGGTGC ATGGAATCCCTG ACGTTACAACCC ATCGCGCGGGTC GATGGCGCCATT AATTTACCTGGC
          S   K   S   V   S   N   R   A   L   L   L   A   A   L   A   C   G   K   T   A   L   T   N   L
4497   TCCAAAAGTGTT TCAAACCGTGCT TTGCTCCTGGCG GCTTTAGCTTGT GGTAAAACCGCT CTGACGAATCTG
          L   D   S   D   D   V   R   H   M   L   N   A   L   S   A   L   G   I   N   Y   T   L   S   A
4569   CTGGATAGCGAT GACGTCCGCCAT ATGCTCAATGCC CTGAGCGCGTTG GGGATCAATTAC ACCCTTTCTGCC
          D   R   T   R   C   D   I   T   G   N   G   G   A   L   R   A   P   G   A   L   E   L   F   L
4641   GATCGCACCCGC TGTGATATCACG GGTAATGGCGGC GCATTACGTGCG CCAGGCGCTCTG GAACTGTTTCTC
          G   N   A   G   ▮   A   M   R   S   L   A   A   A   L   C   L   G   Q   N   E   I   V   L   T
4713   GGTAATGCCGGA ACCGCGATGCGT TCGTTAGCGGCA GCGCTATGTCTG GGGCAAAATGAG ATAGTGTTAACC
          G   E   P   R   M   K   E   R   P   I   G   H   L   V   D   S   L   R   Q   G   G   A   N   I
4785   GGCGAACCGCGT ATGAAAGAGCGT CCGATAGGCCAT CTGGTCGATTCG CTGCGTCAGGGC GGGGCGAATATT
          D   Y   L   E   Q   E   N   Y   P   P   L   R   L   R   G   G   F   T   G   G   D   I   E   V
4857   GATTACCTGGAG CAGGAAAACTAT CCGCCCCTGCGT CTGCGCGGCGGT TTTACCGGCGGC GACATTGAGGTT
          D   G   S   V   S   S   Q   F   L   T   A   L   L   M   T   A   P   L   A   P   K   D   T   I
4929   GATGGTAGCGTT TCCAGCCAGTTC CTGACCGCTCTG CTGATGACGGCG CCGCTGGCCCCT AAAGACACAATT
                                                            ClaI
                                                            ------
          I   R   V   K   G   E   L   V   S   K   P   Y   I   D   I   T   L   N   L   M   K   T   F   G
5001   ATTCGCGTTAAA GGCGAACTGGTA TCAAAACCTTAC ATCGATATCACG CTAAATTTAATG AAAACCTTTGGC
          V   E   I   A   N   H   H   Y   Q   Q   F   V   V   K   G   G   Q   Q   Y   H   S   P   G   R
5073   GTGGAGATAGCG AACCACCACTAC CAACAATTTGTC GTGAAGGGAGGT CAACAGTATCAC TCTCCAGGTCGC
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            Y  L  V  E     G  D  A  S     S  A  S  Y     F  L  A  A     G  A  I  K     G  G  T  V
5145   TATCTGGTCGAG  GGCGATGCCTCG  TCAGCGTCCTAT  TTTCTCGCCGCT  GGGGCGATAAAA  GGCGGCACGGTA
            K  V  T  G     I  G  R  K     S  M  Q  G     D  I  R  F     A  D  V  L     E  K  M  G
5217   AAAGTGACCGGA  ATTGGCCGCAAA  AGTATGCAGGGC  GATATTCGTTTT  GCCGATGTGCTG  GAGAAAATGGGC
            A  T  I  T     W  G  D  D     F  I  A  C     T  R  G  E     L  H  A  I     D  M  D  M
5289   GCGACCATTACC  TGGGGCGATGAT  TTTATTGCCTGC  ACGCGCGGTGAA  TTGCACGCCATA  GATATGGATATG
            N  H  I  P     D  A  A  M     T  I  A  T     T  A  L  F     A  K  G  T     T  T  L  R
5361   AACCATATTCCG  GATGCGGCGATG  ACGATTGCCACC  ACGGCGCTGTTT  GCGAAAGGAACC  ACGACGTTGCGC
            N  I  Y  N     W  R  V  K     E  T  D  R     L  F  A  M     A  T  E  L     R  K  V  G
5433   AATATTTATAAC  TGGCGAGTGAAA  GAAACCGATCGC  CTGTTCGCGATG  GCGACCGAGCTA  CGTAAAGTGGGC
            A  E  V  E     E  G  H  D     Y  I  R  I     T  P  P  A     K  L  Q  H     A  D  I  G
5505   GCTGAAGTCGAA  GAAGGGCACGAC  TATATTCGTATC  ACGCCGCCGGCG  AAGCTCCAACAC  GCGGATATTGGC
            T  Y  N  D     H  R  M  A     M  C  F  S     L  V  A  L     S  D  T  P     V  T  I  L
5577   ACGTACAACGAC  CACCGTATGGCG  ATGTGCTTCTCA  CTGGTCGCACTG  TCCGATACGCCA  GTTACGATCCTG
            D  P  K  C     T  A  K  T     F  P  D  Y     F  E  Q  L     A  R  M  S     T  P  A
5649   GACCCTAAATGT  ACCGCAAAAACG  TTCCCTGATTAT  TTCGAACAACTG  GCGCGAATGAGT  ACGCCTGCC
```

Exhibit 4

Fragment of pCH 91
3329 bp (molecule 6024 bp)

Coding sequence for pCH91:

```
          M   A   S   I   S   S   S   V   A   T   V   S   R   T   A   P   A   Q   A   N   M   V   A   P
5363   ATGGCTTCGATC TCCTCCTCAGTC GCGACCGTTAGC CGGACCGCCCCT GCTCAGGCCAAC ATGGTGGCTCCG
          F   T   G   L   K   S   N   A   A   F   P   T   T   K   K   A   N   D   F   S   T   L   P   S
5435   TTCACCGGCCTT AAGTCCAACGCC GCCTTCCCCACC ACCAAGAAGGCT AACGACTTCTCC ACCCTTCCCAGC
          N   G   G   R   V   Q   C   M   Q   V   W   P   A   Y   G   N   K   K   F   E   T   L   S   Y
5507   AACGGTGGAAGA GTTCAATGTATG CAGGTGTGGCCG GCCTACGGCAAC AAGAAGTTCGAG ACGCTGTCGTAC
          L   P   P   L   S   M   A   P   T   V   M   M   A   S   S   A   T   A   V   A   P   F   Q   G
5579   CTGCCGCCGCTG TCTATGGCGCCC ACCGTGATGATG GCCTCGTCGGCC ACCGCCGTCGCT CCGTTCCAGGGG
          L   K   S   T   A   S   L   P   V   A   R   R   S   S   R   S   L   G   N   V   S   N   G   G
5651   CTCAAGTCCACC GCCAGCCTCCCC GTCGCCCGCCGC TCCTCCAGAAGC CTCGGCAACGTC AGCAACGGCGGA
          R   I   R   C   M   E   S   L   T   L   Q   P   I   A   R   V   D   G   A   I   N   L   P   G
5723   AGGATCCGGTGC ATGGAATCCCTG ACGTTACAACCC ATCGCGCGGGTC GATGGCGCCATT AATTTACCTGGC
          S   K   S   V   S   N   R   A   L   L   L   A   A   L   A   C   G   K   T   A   L   T   N   L
5795   TCCAAAAGTGTT TCAAACCGTGCT TTGCTCCTGGCG GCTTTAGCTTGT GGTAAAACCGCT CTGACGAATCTG
          L   D   S   D   D   V   R   H   M   L   N   A   L   S   A   L   G   I   N   Y   T   L   S   A
5867   CTGGATAGCGAT GACGTCCGCCAT ATGCTCAATGCC CTGAGCGCGTTG GGGATCAATTAC ACCCTTTCTGCC
          D   R   T   R   C   D   I   T   G   N   G   G   A   L   R   A   P   G   A   L   E   L   F   L
5939   GATCGCACCCGC TGTGATATCACG GGTAATGGCGGC GCATTACGTGCG CCAGGCGCTCTG GAACTGTTTCTC
          G   N   A   G   I   A   M   R   S   L   A   A   A   L   C   L   G   Q   N   E   I   V   L   T
6011   GGTAATGCCGGA ATCGCGATGCGT TCGTTAGCGGCA GCGCTATGTCTG GGGCAAAATGAG ATAGTGTTAACC
          G   E   P   R   M   K   E   R   P   I   G   H   L   V   D   S   L   R   Q   G   G   A   N   I
  59   GGCGAACCGCGT ATGAAAGAGCGT CCGATAGGCCAT CTGGTCGATTCG CTGCGTCAGGGC GGGGCGAATATT
          D   Y   L   E   Q   E   N   Y   P   P   L   R   L   R   G   G   F   T   G   G   D   I   E   V
 131   GATTACCTGGAG CAGGAAAACTAT CCGCCCCTGCGT CTGCGCGGCGGT TTTACCGGCGGC GACATTGAGGTT
          D   G   S   V   S   S   Q   F   L   T   A   L   L   M   T   A   P   L   A   P   K   D   T   I
 203   GATGGTAGCGTT TCCAGCCAGTTC CTGACCGCTCTG CTGATGACGGCG CCGCTGGCCCCT AAAGACACAATT
          I   R   V   K   G   E   L   V   S   K   P   Y   I   D   I   T   L   N   L   M   K   T   F   G
 275   ATTCGCGTTAAA GGCGAACTGGTA TCAAAACCTTAC ATCGATATCACG CTAAATTTAATG AAAACCTTTGGC
          V   E   I   A   N   H   H   Y   Q   Q   F   V   V   K   G   G   Q   Q   Y   H   S   P   G   R
 347   GTGGAGATAGCG AACCACCACTAC CAACAATTTGTC GTGAAGGGAGGT CAACAGTATCAC TCTCCAGGTCGC
          Y   L   V   E   G   D   A   S   S   A   S   Y   F   L   A   A   G   A   I   K   G   G   T   V
 419   TATCTGGTCGAG GGCGATGCCTCG TCAGCGTCCTAT TTTCTCGCCGCT GGGGCGATAAAA GGCGGCACGGTA
          K   V   T   G   I   G   R   K   S   M   Q   G   D   I   R   F   A   D   V   L   E   K   M   G
 491   AAAGTGACCGGA ATTGGCCGCAAA AGTATGCAGGGC GATATTCGTTTT GCCGATGTGCTG GAGAAAATGGGC
          A   T   I   T   W   G   D   D   F   I   A   C   T   R   G   E   L   H   A   I   D   M   D   M
 563   GCGACCATTACC TGGGGCGATGAT TTTATTGCCTGC ACGCGCGGTGAA TTGCACGCCATA GATATGGATATG
          N   H   I   P   D   A   A   M   T   I   A   T   T   A   L   F   A   K   G   T   T   T   L   R
 635   AACCATATTCCG GATGCGGCGATG ACGATTGCCACC ACGGCGCTGTTT GCGAAAGGAACC ACGACGTTGCGC
```

```
       N   I   Y   N     W   R   V   K     E   T   D   R     L   F   A   M     A   T   E   L     R   K   V   G
707  AATATTTATAAC TGGCGAGTGAAA GAAACCGATCGC CTGTTCGCGATG GCGACCGAGCTA CGTAAAGTGGGC
       A   E   V   E     E   G   H   D     Y   I   R   I     T   P   P   A     K   L   Q   H     A   D   I   G
779  GCTGAAGTCGAA GAAGGGCACGAC TATATTCGTATC ACGCCGCCGGCG AAGCTCCAACAC GCGGATATTGGC
       T   Y   N   D     H   R   M   A     M   C   F   S     L   V   A   L     S   D   T   P     V   T   I   L
851  ACGTACAACGAC CACCGTATGGCG ATGTGCTTCTCA CTGGTCGCACTG TCCGATACGCCA GTTACGATCCTG
       D   P   K   C     T   A   K   T     F   P   D   Y     F   E   Q   L     A   R   M   S     T   P   A
923  GACCCTAAATGT ACCGCAAAAACG TTCCCTGATTAT TTCGAACAACTG GCGCGAATGAGT ACGCCTGCC
```

Exhibit 5: OTP - DMMG
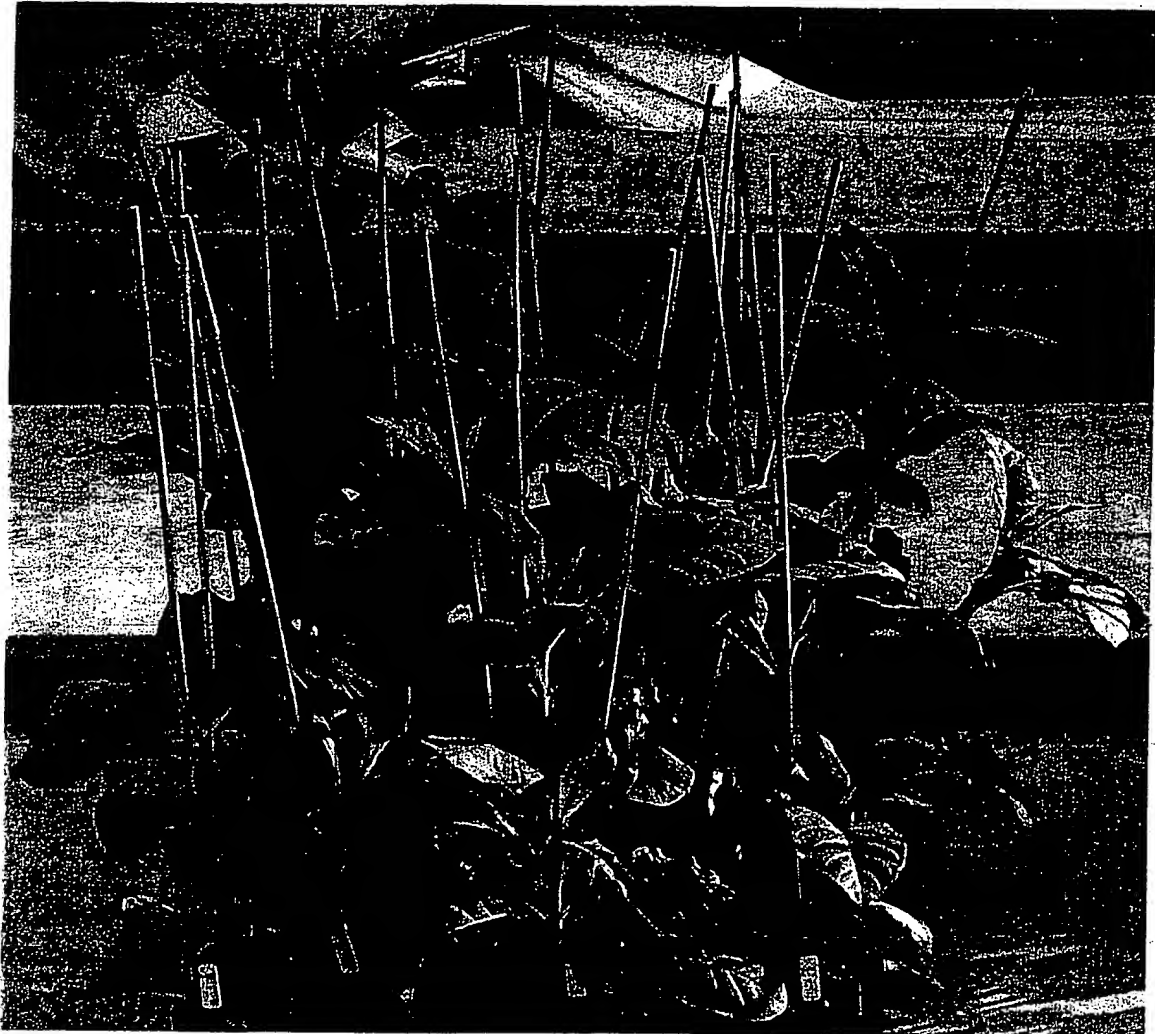
Exhibit 6: TPha+22AAmz - DMMG

Exhibit 7: OTP - DMAroA

Exhibit 8:
Comparison OTP-DMMG (left) and TPha+22AAmz-DMMG (right)

Exhibit 9:
Comparison OTP - DMMG (left) v. OTP - DMAroA (right)

Exhibit 10:
OTP-DMMG (left); OTP-DMAroA; and TPha+22AAmz-DMMG (right)